

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
OM protein - protein search, using sw model

Run on: August 28, 2003, 18:25:32 ; Search time 5.66667 Seconds
Perfect score: 62
Sequence: US-09-743-225-4
1 RDKATFFGHDG 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	56	90.3	345	1	APOH_HUMAN	P02749 homo sapien
2	46	74.2	345	1	APOH_MOUSE	Q01339 mus musculus
3	42	67.7	1310	1	YB35_SCOPD	Q14340 schizosaccharomyces pombe
4	41	66.1	297	1	APOH_RAT	P26644 rattus norvegicus
5	41	66.1	345	1	APOH_CANFA	P33703 canis familiaris
6	40	64.5	345	1	APOH_BOVIN	P17690 bos taurus
7	40	64.5	363	1	DP3B_SPICI	P34029 spiroplasma
8	38	61.3	283	1	FL123_CORE	074631 coriolus ve
9	37	59.7	537	1	DEXB_STREQ	059905 streptococcus
10	36	58.1	307	1	Y650_VIBCH	Q9ku39 vibrio cholerae
11	36	58.1	417	1	TRMO_YEAST	Q12093 saccharomyces cerevisiae
12	36	58.1	477	1	F1BB_PETRA	P02678 petromyzon marinus
13	36	58.1	496	1	CWBL_BACSU	Q02114 bacillus subtilis
14	36	58.1	798	1	PHSG_BACSU	P39123 bacillus subtilis
15	36	58.1	964	1	UL70_MCMVS	Q69153 murine cytomegalovirus
16	35	56.5	198	1	IFP2_ARATH	Q04663 arabidopsis thaliana
17	35	56.5	241	1	PYRH_HAFLN1	Q9hn83 halobacter
18	35	56.5	574	1	SYR_BUCA1	Q44683 buchnera apertifolia
19	35	56.5	962	1	UL5_PRVKA	Q85228 pseudoradulara
20	35	56.5	2209	1	KNTB_HUMAN	P50748 homo sapiens
21	34	54.8	151	1	GLB6_CHITTH	P02227 chironomus
22	34	54.8	162	1	GLB6_CHITTH	P02224 chironomus
23	34	54.8	366	1	QUBA_CAOCR	Q9a7y2 caulobacter
24	34	54.8	373	1	YSAK_CAEEL	Q93454 caenorhabditis elegans
25	34	54.8	398	1	CGL_MOUSE	Q8vcn5 mus musculus
26	34	54.8	415	1	RF11_METFAC	Q8tbm4 methanospirillum
27	34	54.8	418	1	YMF13_YEAST	Q04526 saccharomyces cerevisiae
28	34	54.8	644	1	XIND_CELL1	P54865 cellulomonas
29	34	54.8	699	1	MALO_HAZIN	P45176 haemophilus ducreyi
30	34	54.8	937	1	SYL_ECOLI	P00956 escherichia coli
31	34	54.8	973	1	UVRA_RHIME	P56899 rhizobium m
32	33	53.2	145	1	GLB7_CHITTH	P02226 chironomus
33	33	53.2	161	1	GLB9_CHITTH	P02223 chironomus

ALIGNMENTS

34	33	53.2	162	1	GLBH_CHITH	P12550 chironomus
35	33	53.2	162	1	GLBH_CHITP	P29242 chironomus
36	33	53.2	349	1	ALFL_CHLPN	Q9z8q7 chlamydia pneumoniae
37	33	53.2	398	1	TRMU_BRDME	P8y116 brucella melitaei
38	33	53.2	430	1	MAS1_JGRT9	P50202 agrobacteriophage
39	33	53.2	475	1	EX1_ECOLI	P04995 escherichia coli
40	33	53.2	505	1	SM11_YEAST	P52911 saccharomyces cerevisiae
41	33	53.2	505	1	EXG2_YEAST	P26309 saccharomyces
42	33	53.2	610	1	CC20_YEAST	P26309 saccharomyces
43	33	53.2	713	1	CDG2_PAEM	P21835 paenibacillus
44	33	53.2	921	1	SVT1_BACSU	Q45477 bacillus suaveolens
45	33	53.2	923	1	AGLU_TETPY	P00906 tetrahymena thermophila

AC	33	53.2	162	1	GLBH_CHITH	P12550 chironomus
DT	33	53.2	349	1	ALFL_CHLPN	P29242 chironomus
DT	33	53.2	398	1	TRMU_BRDME	Q8y116 brucella melitaei
DT	33	53.2	430	1	MAS1_JGRT9	P50202 agrobacteriophage
DE	33	53.2	475	1	EX1_ECOLI	P04995 escherichia coli
DB	33	53.2	505	1	SM11_YEAST	P52911 saccharomyces cerevisiae
DB	33	53.2	505	1	EXG2_YEAST	P26309 saccharomyces
DB	33	53.2	610	1	CC20_YEAST	P26309 saccharomyces
GN	33	53.2	713	1	CDG2_PAEM	P21835 paenibacillus
OS	33	53.2	921	1	SVT1_BACSU	Q45477 bacillus suaveolens
OC	33	53.2	923	1	AGLU_TETPY	P00906 tetrahymena thermophila
OX	33	53.2	923	1	GLBH_CHITH	P12550 chironomus
RN	33	53.2	923	1	GLBH_CHITP	P29242 chironomus
RP	33	53.2	923	1	ALFL_CHLPN	P29242 chironomus
RC	33	53.2	923	1	TRMU_BRDME	Q8y116 brucella melitaei
RX	33	53.2	923	1	MAS1_JGRT9	P50202 agrobacteriophage
RA	33	53.2	923	1	EX1_ECOLI	P04995 escherichia coli
RA	33	53.2	923	1	SM11_YEAST	P52911 saccharomyces cerevisiae
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RP	33	53.2	923	1	GLBH_CHITH	P12550 chironomus
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RA	33	53.2	923	1	AGLU_TETPY	P00906 tetrahymena thermophila
RT	33	53.2	923	1	GLBH_CHITH	P12550 chironomus
RT	33	53.2	923	1	ALFL_CHLPN	P29242 chironomus
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RT	33	53.2	923	1	GLBH_CHITH	P12550 chironomus
RT	33	53.2	923	1	ALFL_CHLPN	P29242 chironomus
RT	33	53.2	923	1	TRMU_BRDME	Q8y116 brucella melitaei

RA	Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;	-1- SIMILARITY: Contains 4 Sushi (SCR) domains.
RL	"The genome sequence of Schizosaccharomyces pombe.";	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-1- SIMILARITY: BELONGS TO THE OSBP FAMILY.	CC
CC	-1- SIMILARITY: Contains 1 PH repeats.	CC
CC	-1- SIMILARITY: Contains 3 ANK repeats.	CC
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC
CC	-1- SIMILARITY: Contains 1 PH domain.	CC
CC	-1- SIMILARITY: Contains 3 ANK repeats.	CC
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC
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CC	-1- SIMILARITY: Contains 4 Sushi (SCR) domains.	CC
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DR	Z97211; CB10154-2;	DR X15551; CAA33556-1; -.
DR	PIR; T40135; T40135.	DR S05310; NBNT.
DR	GeneDB_Spondie; SPBC2P12:05c; -.	DR HSSP; P02749; 1C12.
DR	InterPro; IPR002110; ANK.	DR InterPro; IPR00436; Sushi_SCR_CCP.
DR	InterPro; IPR006648; Oxysterol_BP.	DR Pfam; PF00084; sushi; 3.
DR	InterPro; IPR00849; PH.	DR SMART; SM00032; CCP; 3.
DR	Pfam; PF0023; ank; 3.	DR Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.
DR	Pfam; PE01237; Oxysterol_BP; 1.	DR SIGNAL; 1
DR	Pfam; PF00169; PH; 1.	FT CHAIN; 20
DR	SMART; SM00248; ANK; 3.	FT DOMAIN; 20
DR	SMART; SM00233; PH; 1.	FT DOMAIN; 32
DR	PROSITE; PS50088; ANK_REPEAT; 2.	FT DOMAIN; 35
DR	PROSITE; PS5029; ANK_REPEAT; 1.	FT DOMAIN; 93
DR	PROSITE; PS0101; OSBP; FALSE_NEG.	FT DOMAIN; 156
DR	PROSITE; PS5000; PH_DOMAIN; 1.	FT DOMAIN; 215
DR	Hypothetical protein; Lipid transport; Transport; ANK repeat; Repeat.	FT DISULFID; 36
FT	REPEAT 54 84 ANK 1.	FT DISULFID; 62
FT	REPEAT 88 118 ANK 2.	FT DISULFID; 94
FT	REPEAT 188 217 ANK 3.	FT DISULFID; 126
FT	DOMAIN 254 349 PH.	FT DISULFID; 157
SQ	SEQUENCE 1310 AA; 148474 MN; E6F284F09C073262 CRC64;	FT DISULFID; 186
Query Match Score 42; DB 1; Length 1310; Best Local Similarity 67.7%; Pred. No. 3.1; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Mismatches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
Qy	2 DKATGFHD 10	Query Match Score 41; DB 1; Length 297; Best Local Similarity 70.0%; Pred. No. 1; Mismatches 1; Indels 0; Gaps 0;
Db	362 DNATGTHD 370	Qy 1 KDRATGFTHD 10 Db 179 KDRATGFCH 188
RESULT 4		
APOR_RAT	STANDARD; PRT; 297 AA.	RESULT 5
ID	P26644;	APOR_CANFA
DT	01-AUG-1992 (Rel. 23, Created)	STANDARD; PRT; 345 AA.
DT	01-FEB-1996 (Rel. 33, Last sequence update)	ID APOR_CANFA
DT	28-FEB-2003 (Rel. 41, Last annotation update)	P3703;
DE	Beta-2-glycoprotein I precursor (Apolipoprotein H) (B2GPI)	AC
DE	(Beta-2GPI).	DT 01-FEB-1994 (Rel. 28, Created)
GN	APOH.	DT 01-FEB-1994 (Rel. 28, Last sequence update)
OS	Rattus norvegicus (Rat).	DT 28-FEB-2003 (Rel. 41, Last annotation update)
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.	DE Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
NCBI_TaxID	10116;	DE (Beta-2GPI).
OX	Canis familiaris (Dog).	GN APOR.
RN	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OS Canis familiaris (Dog).
RP	SEQUENCE FROM N.A.	OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RC	STRAIN-SPECIE-DAWLEY;	OC
RX	MSMLIN=8936680; PubMed=2771654;	NCBI_TaxID=9615;
RA	Aoyama Y.; Chan Y.L.; Woo I.G.;	RN [1]
RT	"The primary structure of rat beta 2-glycoprotein I."	RP SEQUENCE FROM N.A.
RC	Nucleic Acids Res. 17:640-640 (1988).	RC STRAIN=Beagle; TISSUE=Liver;
CC	-1- FUNCTION: Binds to various kinds of negatively charged substances such as heparin, phospholipids, and dextran sulfate, may prevent activation of the intrinsic blood coagulation cascade by binding	RX MEDLINE=93221500; PubMed=7682067;
CC	to phospholipids on the surface of damaged cells.	RA Seller G.C., Keane J., Mahdi H., Peeples M.E., Browne N., Whitehead A.S.;
CC	-1- SUBCELLULAR LOCATION: Secreted.	RT "Characterization and acute phase modulation of canine apolipoprotein H (beta 2-glycoprotein I).";
CC	-1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.	RT Biochem. Biophys. Res. Commun. 191:1288-1293 (1993).
CC	-1- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES	CC

SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.

-|- SUBCELLULAR LOCATION: Secreted.

-|- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.

-|- SIMILARITY: Contains 4 Sushi (SCR) domains.

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CC EMBL; X72933; CAA51438.1; -.

DR PIR; JN0465; JN0465.

DR HSSP; P02749; 1C1Z.

DR InterPro; IPR00336; Sushi_SCR_CCP.

DR Pfam; PF00084; sushi; 4.

DR SMART; SM00032; CCP; 4.

RW Receptor-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.

FT SIGNAL_1 19 BY SIMILARITY.

FT CHAIN 20 345 BEPA-2-GLYCOPROTEIN I.

FT DOMAIN 22 80 SUSHI 1.

FT DOMAIN 83 138 SUSHI 2.

FT DOMAIN 141 201 SUSHI 3.

FT DOMAIN 204 261 SUSHI 4.

FT DOMAIN 263 345 SUSHI-LIKE.

FT DISULFID 23 66 BY SIMILARITY.

FT DISULFID 51 79 BY SIMILARITY.

FT DISULFID 84 124 BY SIMILARITY.

FT DISULFID 110 137 BY SIMILARITY.

FT DISULFID 142 188 BY SIMILARITY.

FT DISULFID 174 200 BY SIMILARITY.

FT DISULFID 205 248 BY SIMILARITY.

FT DISULFID 234 260 BY SIMILARITY.

FT DISULFID 264 315 BY SIMILARITY.

FT DISULFID 300 325 BY SIMILARITY.

FT DISULFID 307 345 BY SIMILARITY.

FT CARBOHYD 117 117 N'-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 162 162 N'-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 183 183 N'-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 193 193 N'-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 253 253 N'-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 345 AA; 38:03 MW; EOB2624879B/4FEA CRC64;

Query Match 66.18; Score 41; DB 1; Length 345;

Best Local Similarity 70.0%; Pred. No. 1.2;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 10

DB 227 KDKAMYGCHD 236

RESULT 6

AP0H_BOVIN AP0H_BOVIN STANDARD; PRT; 345 AA.

ID AP0H_BOVIN P17630; Q28052;

AC P17630; Q28052;

DT 01-NOV-1990 (Rel. 15, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI) (Beta(2)GPI).

GN AP0H.

OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.

NCBI_TAXID=9913;

[1] SEQUENCE FROM N.A.

RP

CC TISSUE-Liver; Gao B.; Virmanni M.; Romm E.; Lazar-Wesley E.; Sakaguchi K., Appella E.; Kunos G.; Takacs L.; Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.

CC TISSUE-Liver; SEQUENCE OF 4-345 FROM N.A.; PARTIAL SEQUENCE, AND DISULFIDE BONDS.

CC TISSUE-Liver; RP SEQUENCE OF 4-345 FROM N.A.; PARTIAL SEQUENCE, AND DISULFIDE BONDS.

CC TISSUE-Liver; RX MEDLINE=92232647; PubMed=1567819;

CC TISSUE-Liver; RA Bendixen B.; Halkier T.; Magnusson S.; Sottrup-Jensen L., Kristensen T.; "Complete primary structure of bovine beta 2-glycoprotein I: localization of the disulfide bridges." Biochemistry 31:3611-3617(1992).

CC TISSUE-Liver; RN [3]

CC TISSUE-Plasma; RP SEQUENCE OF 20-345, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.

CC TISSUE-Plasma; RX MEDLINE=92089075; PubMed=1751487;

CC TISSUE-Plasma; RA Kato H.; Enyoyaji K.-I.; "Amino acid sequence and location of the disulfide bonds in bovine beta 2 glycoprotein I: the presence of five Sushi domains." Biochemistry 30:11687-11694(1991).

CC TISSUE-Plasma; RN [4]

CC TISSUE-Plasma; RP SEQUENCE OF 20-41; RX MEDLINE=90226328; PubMed=2327984;

CC TISSUE-Plasma; RA L1 Q.; Blacher R.; Esch F.; Conote L.F.; "Isolation from fetal bovine serum of an apolipoprotein-H-like protein which inhibits thymidine incorporation in fetal calf erythroid cells." Biochem. J. 267:261-264(1990).

CC TISSUE-Plasma; RT "FUNCTION: Binds to various kinds of negatively charged substances such as heparin, phospholipids, and dextran sulfate. May prevent activation of the intrinsic blood coagulation cascade by binding to phospholipids on the surface of damaged cells."

CC TISSUE-Plasma; RT "-1- FUNCTION: Secreted.

CC TISSUE-Plasma; RT "-1- SUBCELLULAR LOCATION: Secreted.

CC TISSUE-Plasma; RT "-1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.

CC TISSUE-Plasma; RT "-1- SIMILARITY: Contains 4 Sushi (SCR) domains.

CC TISSUE-Plasma; RT This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC TISSUE-Plasma; DR EMBL; L07303; AAA30382 1; -.

CC TISSUE-Plasma; DR EMBL; X60065; CA42669 1; -.

CC TISSUE-Plasma; DR PIR; JN0502; NBBO.

CC TISSUE-Plasma; DR InterPro; IP0000436; Sushi_SCR_CCP.

CC TISSUE-Plasma; DR Pfam; PF00084; sushi; 4.

CC TISSUE-Plasma; DR SM00032; CCP; 4.

CC TISSUE-Plasma; DR Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.

CC TISSUE-Plasma; FT CHAIN 1 19 BETA-2-GLYCOPROTEIN I.

CC TISSUE-Plasma; FT DOMAIN 20 345 SUSHI 1.

CC TISSUE-Plasma; FT DOMAIN 22 80 SUSHI 2.

CC TISSUE-Plasma; FT DOMAIN 83 138 SUSHI 3.

CC TISSUE-Plasma; FT DOMAIN 141 201 SUSHI 4.

CC TISSUE-Plasma; FT DOMAIN 204 261 SUSHI-LIKE.

CC TISSUE-Plasma; FT DOMAIN 263 345 SUSHI-LIKE.

CC TISSUE-Plasma; FT DOMAIN 264 315 SUSHI-LIKE.

CC TISSUE-Plasma; FT DOMAIN 300 325 SUSHI-LIKE.

CC TISSUE-Plasma; FT DOMAIN 307 345 SUSHI-LIKE.

CC TISSUE-Plasma; FT CARBOHYD 117 117 N'-LINKED (GLCNAC. . .) (POTENTIAL).

CC TISSUE-Plasma; FT CARBOHYD 162 162 N'-LINKED (GLCNAC. . .) (POTENTIAL).

CC TISSUE-Plasma; FT CARBOHYD 183 183 N'-LINKED (GLCNAC. . .) (POTENTIAL).

CC TISSUE-Plasma; FT CARBOHYD 193 193 N'-LINKED (GLCNAC. . .) (POTENTIAL).

CC TISSUE-Plasma; FT CARBOHYD 253 253 N'-LINKED (GLCNAC. . .) (POTENTIAL).

CC TISSUE-Plasma; FT SEQUENCE 345 AA; 38:03 MW; EOB2624879B/4FEA CRC64;

CC TISSUE-Plasma; FT SIGNAL 1 19 BETA-2-GLYCOPROTEIN I.

CC TISSUE-Plasma; FT DOMAIN 20 345 SUSHI 1.

CC TISSUE-Plasma; FT DOMAIN 22 80 SUSHI 2.

CC TISSUE-Plasma; FT DOMAIN 83 138 SUSHI 3.

CC TISSUE-Plasma; FT DOMAIN 141 201 SUSHI 4.

CC TISSUE-Plasma; FT DOMAIN 204 261 SUSHI-LIKE.

CC TISSUE-Plasma; FT DOMAIN 263 345 SUSHI-LIKE.

CC TISSUE-Plasma; FT DISULFID 23 66

CC TISSUE-Plasma; FT DISULFID 51 79

CC TISSUE-Plasma; FT DISULFID 84 124

CC TISSUE-Plasma; FT DISULFID 110 137

CC TISSUE-Plasma; FT DISULFID 142 188

CC TISSUE-Plasma; FT DISULFID 174 200

CC TISSUE-Plasma; FT DISULFID 205 248

CC TISSUE-Plasma; FT DISULFID 234 260

CC TISSUE-Plasma; FT DISULFID 264 315

CC TISSUE-Plasma; FT DISULFID 300 325

CC TISSUE-Plasma; FT DISULFID 307 345

CC TISSUE-Plasma; FT CARBOHYD 92 92

CC TISSUE-Plasma; FT CARBOHYD 162 162

CARBOHYD	183	183	N-LINKED (GLCNAC. .).	DR Pfam; PF02767; DNA_P013_beta_2; 1.
CARBONYD	193	193	N-LINKED (GLCNAC. .).	DR Pfam; PF02768; DNA_P013_beta_3; 1.
CARBONYD	253	253	N-LINKED (GLCNAC. .).	DR SMART; SM00480; POL3BC; 1.
CONFLICT	101	101	E -> G (IN REF. 1).	DR TIGREAMS; TIGR0663; dnan; 1.
CONFLICT	108	108	F -> S (IN REF. 1).	KW TRANSFERASE; DNA-directed DNA polymerase; DNA replication.
CONFLICT	177	177	H -> R (IN REF. 1).	SO SEQUENCE 363 AA; 41339 MW; C99A39BEF6D6 CRC64;
CONFLICT	191	191	H -> N (IN REF. 3).	Query Match 64.5%; Score 40; DB 1; Length 363;
CONFLICT	194	194	W -> C (IN REF. 1).	Best Local Similarity 72.7%; Pred. No. 2;
CONFLICT	259	259	S -> N (IN REF. 1).	Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CONFLICT	302	302	H -> N (IN REF. 1).	
CONFLICT	305	305	K -> R (IN REF. 1).	
CONFLICT	329	329	H -> R (IN REF. 1).	
SEQUENCE	345 AA;	38252 MW;	E117DAB609461C33 CRC64;	QY 1 KDKATFGTHD 11
				DB 39 RDKTTFITSDG 49
RESULT 8				
DP3B_SPICI	STANDARD;	PRT;	283 AA.	ID F112_CORYNE STANDARD; PRT;
P34029;	1	KDATFGTHD 10		ID F112_CORYNE
	1 1 1 :			AC 074631;
	227	KDATFGCHE 236		DT 30-MAY-2000 (Rel. 39, Created)
RESULT 7				
DP3B_SPICI	STANDARD;	PRT;	363 AA.	DT 30-MAY-2000 (Rel. 39, Last sequence update)
P34029;	1	KDATFGTHD 10		DT 30-MAY-2000 (Rel. 39, Last annotation update)
01-FEB-1994	(Rel. 28, Created)			DE Protein FDD123 (CvHSP30/1).
01-FEB-1994	(Rel. 28, Last sequence update)			GN FDD123.
28-FEB-2003	(Rel. 41, Last annotation update)			GN
DNA Polymerase III, beta chain (EC 2.7.7.7).				OS Corynus versicolor.
DNA.				OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Spiroplasma citri.				OC Aphylophorales; Coriolus.
Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;				NCBI_TaxID=5746;
Spiroplasmataceae; Spiroplasma.				RN [1]
[1]				RP SEQUENCE FROM N.A.
STRAIN=R8A21P;				RC STRAIN=IFO 303440;
MEDLINE=94280261; PubMed=7764984;				RX MEDLINE=97398356; PubMed=9256254;
re F., Renaudin J., Bove J.M., Laigret F.;				RA Imura Y., Tasbumi K.;
"Cloning and sequencing of the replication origin (oriC) of the				RT "Isolation of mRNAs induced by a hazardous chemical in white-rot
Spiroplasma citri chromosome and construction of autonomously				fungus, Coriolus versicolor, by differential display.";
replicating artificial plasmids";				RL FEBS Lett. 412:370-374 (1997).
Curr. Microbiol. 29:23-29 (1994).				CC -1 SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME				CC -1 SIMILARITY: BELONGS TO THE ARCHAEL OPSIN FAMILY. HSP30
RESPONSIVE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.				CC
THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.				CC
THE BETA CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT				CC
IS CLAMPED ONTO DNA, IT SLIDES FREELY (BIDIRECTIONAL AND ATP-				CC
INDEPENDENT) ALONG DUPLEX DNA (BY SIMILARITY).				CC
-1- CATALYTIC ACTIVITY: N deoxyribonucleoside triphosphate = N diphosphate				CC
+ (DNA) (N).				CC
-1- SUBUNIT: DNA POLYMERASE III contains a core (composed of alpha,				CC
epsilon and theta chains) that associates with a tau subunit. This				CC
core dimerizes to form the POLIII complex. POLIII associates				CC
with the gamma complex (composed of gamma, delta, delta', psi and				CC
chi chains) and with the beta chain to form the complete DNA				CC
POLYMERASE III complex (By similarity).				CC
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).				CC
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the European Bioinformatics Institute. There are no restrictions on its				CC
use by non-profit institutions as long as its content is in no way				CC
modified and this statement is not removed. Usage by and for commercial				CC
entities requires a license agreement (See http://www.isb-sib.ch/announce/				CC
or send an email to license@isb-sib.ch).				CC
EMBL; Z19108; CAM33; S35733; InterPro; IP001001; PIR; S35733; Pfam; PF00742; DNA_P013_beta_1; -.				CC
InterPro; IP001001; DNA_P013_beta_1; -.				CC
Pfam; PF00742; DNA_P013_beta_1; -.				CC
InterPro; IP001001; DNA_P013_beta_1; -.				CC
Query Match 61.3%; Score 38; DB 1; Length 283;				CC
Best Local Similarity 70.0%; Pred. No. 3.8;				CC
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				CC
2 DKAFTGTHD_11				CC

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CC EMBL; 271781; CAA98591.1;

DR PIR; S67566; S67566.

DR SGD; S000219.; YD033C.

DR InterPro; IPR004506; TrmU.

DR Pfam; PP0305.; tRNA_Me_trans; 1.

DR TIGRFAMS; TIGR0020; trmU; 1.

KW transerase; Methyltransferase; tRNA processing.

SQ SEQUENCE 417 AA; 47049 MW; 15BF65FD9A094890 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 417;

Best Local Similarity 66.7%; Pred. No. 14;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KATFGTHDG 11

| :| |||

Db 264 KTWTGHRDG 272

RESULT 12

FIBB_PETM A STANDARD; PRT; 477 AA.

AC P01678;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Fibronogen beta chain [Contains: Fibrinopeptide B] (Fragments).

OS Petromyzon marinus (Sea lamprey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

OC Petromyzontiformes; Petromyzontidae; Petromyzon.

NCBI_TaxID:7757;

OX [1]

RN SEQUENCE OF 1-36;

RP MEDLINE-77055679; PubMed-999898;

RA Cotterell B.A.; Doolittle R.F.;

RT "Amino acid sequences of lamprey fibrinopeptides A and B and characterizations of the junctions split by lamprey and mammalian thrombins.";

RT Biochim. Biophys. Acta 453:426-438(1976).

RN [2]

RP SEQUENCE OF 37-477 FROM N.A.

RA MEDLINE-87076582; PubMed-3190537;

RA Bonhous V.L.; Doolittle R.F.; Pontes M.; Strong D.D.;

RT Biochemistry 25:6512-6516(1986).

CC -1 FUNCTION: FIBRINogen HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.

CC -1 SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

CC *Complementary DNA sequence of lamprey fibrinogen beta chain.;"

CC -1 FUNCTION: FIBRINogen HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.

CC -1 SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC -1 MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIa, WHICH CATALIZES THE CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT

CC MONOMERS.

CC -1 SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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CC or send an email to license@isb-sib.ch).

CC DR M14773; AAA49261.1;

CC

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CC EMBL; 274081; CAA98591.1;

DR PIR; S67566; S67566.

DR SGD; S000219.; YD033C.

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DR TIGRFAMS; TIGR0020; trmU; 1.

KW transerase; Methyltransferase; tRNA processing.

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NCBI_TaxID:7757;

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RT "Amino acid sequences of lamprey fibrinopeptides A and B and characterizations of the junctions split by lamprey and mammalian thrombins.";

RT Biochim. Biophys. Acta 453:426-438(1976).

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CC DR M14773; AAA49261.1;

CC

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CC EMBL; 274081; CAA98591.1;

DR PIR; S67566; S67566.

DR SGD; S000219.; YD033C.

DR InterPro; IPR004506; TrmU.

DR Pfam; PP0305.; tRNA_Me_trans; 1.

DR TIGRFAMS; TIGR0020; trmU; 1.

KW transerase; Methyltransferase; tRNA processing.

SQ SEQUENCE 417 AA; 47049 MW; 15BF65FD9A094890 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 417;

Best Local Similarity 66.7%; Pred. No. 14;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KATFGTHDG 11

| :| |||

Db 264 KTWTGHRDG 272

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CC EMBL; 274081; CAA98591.1;

DR PIR; S67566; S67566.

DR SGD; S000219.; YD033C.

DR InterPro; IPR004506; TrmU.

DR Pfam; PP0305.; tRNA_Me_trans; 1.

DR TIGRFAMS; TIGR0020; trmU; 1.

KW transerase; Methyltransferase; tRNA processing.

SQ SEQUENCE 417 AA; 47049 MW; 15BF65FD9A094890 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 417;

Best Local Similarity 66.

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haleij J., Harwood C.R., Heunert A., Hilbert H., Hollsapele S., Hosono S., Hulio M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Klein C., Kobayashi Y., Koeter P., Konigstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Leyne A., Liu H., Masuda S., Maulé C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Oudega B., Park S.H., Parro V., Pohl T.M., Portereil D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purcell B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivoira C., Rocha E., Roche B., Rose M., Sadale Y., Sato T., Scanlan E., Schleicher S., Schroeter R., Scoffone F., Sekiguchi J., Sekova A., Seror S.J., Seirer P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takegiri T., Takemaru K., Takeuchi M., Tamakoshi H., Tanaka T., Terpetra P., Tognoni A., Tosato V., Uchiyama S., Vandenberg M., Vanmer F., Vassarotti A., Viari A., Wambutt R., Wedler B., Weitzeneger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshihikawa H., Zumsalci E., Yoshihikawa H., Zumsalci E., RT

bt1115 :
ture 390:249-256(1997).

- FUNCTION: Autolysins are involved in some important biological processes such as cell separation, cell-wall turnover, competence for genetic transformation, formation of the flagella - in particular of its basal body - and sporulation. Has a high affinity for teichoic acid-endowed Peptidoglycan.
- CATALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl residues and L-amino acid residues in certain bacterial cell-wall glycopeptides.
- SUBCELLULAR LOCATION: Membrane-bound.
- SIMILARITY: BELONGS TO THE N-ACETYLGLURAMOYL-L-ALANINE AMIDASE FAMILY 3.

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CC	EMBL: M87445;	AAA22581.1;	-	
	DR	EMBL: M81324;	AAA22571.1;	
	DR	EMBL: D10388;	BAA01225.1;	
	DR	EMBL: 299322;	CAB15579.1;	-
	PIR:	B41322;	B41322;	
	DR	SubList: BG1407;	LytC.	
	DR	IntersPro: IPR02508;	Amidase_3.	
	DR	Pfam: PF01520;	Amidase_3;	1..
	DR	Pfam: PF01121;	CW_banding_2;	3..
	DR	Pfam: PF00646;	CW_1;	3..
	KW	Competence; Sporulation;	Hydrolase; Cell wall; Membrane;	Repeat;
	KW	Signal; Complete proteome.		
	FT	SIGNAL	1	24
	FT	CHAIN	25	496
	FT	DOMAIN	30	318
	FT	REPEAT	30	128
	FT	REPEAT	129	222
	FT	REPEAT	223	318
	SEQUENCE	496 AA;	52625 MW;	
SO				146FF36BA1BB5EC5 CRC64;

Query Match	Score 36;	DB 1;	Length 496;
Best Local Similarity	58.1%;		
Matched 2.	Score 63.6%;	Pred. No. 17;	Trades
Matches	Conservative	No. Wissmann	A:

Db	RESULT 14	PHSG_BACSU	BACSU	STANDARD;
	ID	PHSG_BACSU		
	AC	P39123;		
	DT	01-FEB-1995	(Rel. 31, Crc	
	DT	01-FEB-1995	(Rel. 31, Lac	
	DT	28-FEB-2003	(Rel. 41, G	
	DE	GLYCOGEN phosphorylase (E		
	GI	Glycogen phosphorylase (E		
	GP	Glycogen phosphorylase (E		
	OS	Bacillus subtilis.		
	OC	Bacteria; Firmicutes; Baa		
	OX	NCBI_TAXID=1423;		
	RN	[1]		
	RP	SEQUENCE FROM N.A.		
	RC	STRAIN=N168;		
	RX	MEDLINE:94195107; PubMed		
	RA	Kiel, J. A. K. W., Boels, J. M.		
	RT	Glycogen In Bacillus sub		
	RT	operon encoding enzymes "		
	RT	degradation";		
	RL	Mol. Microbiol. 11:203-2		
		[2]		

RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98048467; PubMed
 RA Lapidus A., Galleron N.,
 RT "Sequencing and function
 RT in the 200 kb rrnB-dnaB
 RL Microbiology 143:3431-34
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed
 RA Ogasawara N.,
 RA Azeyedo V., Bertero M.G.,
 RA Borrius R., Boursig L.,
 RA Brouillet S., Bruschi C.,
 RA Choi S.K., Codani J.J.,
 RA Denizot F., Deville K.M.,
 RA Entian K.D., Errington J.,
 RA Fultz C., Fujita M., Fuj
 RA Ghim S.Y., Glasser P., Go
 RA Giuseppi G., Guy B.J., Ha

RA	Hilbert H.	Holsappel S.
RA	Joris B.	Karamata D.
RA	Kobayashi Y.	Koetteler P.
RA	Kurita K.	Lapidus A.
RA	Lee S.M.	Liu L.
RA	Medina N.	Mellado R.P.
RA	Noone D.	O'Reilly M.
RA	Patro V.	Pohl T.M.
RA	Presecan E.	Pujic P.
RA	Rieger M.	Rivolta C.
RA	Sato T.	Scanlan B.
RA	Sekiuchi J.	Sekowska A.
RA	Sorkin A.	Tacconi E.
RA	Takemoto M.	Tamashiro A.
RA	Tozato V.	Uchiyama S.
RA	Vizari A.	Wambutt R.
RA	Winters P.	Wipat A.
RA	Yoshida K.	Yoshioka H.
RT	"The complete genome seq submitted."	
RT		

PRM; 798 AR.
 (ed)
 sequence update)
 annotation update)
 2.4.1.1).
 lillales; Bacillaceae; Bacillus.
 145641;
 Beldman G.; Venema G.;
 lillales; molecular characterization
 involved in glycogen biosynthesis
 (1994).

387221; Prokofin A., Ehrlich S.D.; annotation of the *Bacillus suis* strain." (1997).

384377; Albertini A.M., Allon B.; Bassiere P., Botolin A., Borcet M., Brignell S., Cernans A., Braun M., Brignell S., Caldwell B., Capuano V., Carmonerton I.F., Cummings N.J., Dauwsterhoff A., Ehrlich S.D., Fabbret C., Ferrari E., Foulge A.Y., Fuma S., Galizia A., Gallo J., Goughly E.J., Grandi A., Halech J., Harwood C.R.,

Hosono S., Hillo M.F., Itaya M., Klaerr-Blanchard M., Nahara Y., Koenigstein G., Krogh S., Kuma J., Lazarus S., Lauber J., Lazcano C., Medigue S., Masuda S., Mauel C., Meesaki M., Moestl D., Nakai S., Nawa K., Ogihara A., Oudega B., Odeberg D., Porwollik S., Presco, Pernille B., Rapoport G., Rey M., Richa E., Rohe B., Rose M., Sada S., Schroeter R., Scoffone S., Seror S.J., Serror P., Shin B., Takahashi T., Takemoto K., Tanaka T., Terpstra P., Tochio M., Udenbol M., Vannier F., Vassar E., Weder H., Weitzenegger H., Yamamoto H., Yamane K., Yasumoto K., Zumstein E., Yoshikawa H., D. Name of the Gram-positive bacteria

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CC [(1,4)-alpha-D-glucosyl](N-1) + alpha-D-glucose 1-phosphate.
 CC -I- COFACTOR: Pyridoxal phosphate.
 CC -I- INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON
 CC SOURCES THAT ALLOW EFFICIENT SPOORIZATION.
 CC -I- SIMILARITY: BELONGS TO THE GLYCOSYL PHOSPHORYLASE FAMILY.

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 DR EMBL; 235795; CAB01044.1;
 DR EMBL; AF008240; AAC00218.1;
 DR EMBL; 239119; CAB15072.1;
 DR PIR; S40052; S40052.
 DR HSSP; P06738; 1YGP.
 DR SubtilList; BG10911; g1gp.
 DR InterPro; IPR00811; Glyco_trans_35.
 DR Pfam; PF00343; phosphotransferase_1.
 DR PROSITE; PS00102; PHOSPHORYLASE_1.
 KW Transferase; Glycosyltransferase; Allosteric enzyme;
 KW Carbohydrate metabolism; Glycogen metabolism; Pyridoxal phosphate;
 KW Complete proteome;
 FT BINDING 646 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 798 AA; 91755 MW; 2E5FD08F05C75045 CRC94;

Query Match 58.1%; Score 36; DB 1; Length 798;
 Best Local Similarity 85.7%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TFGTHDG 11
 Db 654 TIGTHDG 660

RESULT 15

UL0_MCMV5 STANDARD: PRT: 964 AA.
 ID UL0_MCMV5
 AC 069153;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Helicase/primate complex protein (Probable DNA replication protein
 DE UL70).
 GN UL70.
 OS Murine cytomegalovirus (strain Smith).
 OC Viruses; dsDNA viruses; no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Marmegalovirus.
 OC NCBI_TaxID=10367;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-96082764; PubMed=7483291;
 RA Messerle M., Rapp M., Lucin P., Kozinowski U.H.;
 RT Characterization of a conserved gene block in the murine
 RT cytomegalovirus genome.;
 Virus Genes 10:73-80(1995);

CC -I- FUNCTION: INVOLVED IN DNA REPLICATION (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52;
 CC HSV-1,7, EBV BSLF1, HVS-1,56, VZV 6, HCMV AND MCMV UL70.
 CC -----
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 CC -----
 DR EMBL; L07319; AAA96665.1;
 DR InterPro; IPR004340; UL52_UL70.

DR Pfam; PF03121; UL52_UL70; 1.
 KW Helicase; DNA replication.
 SQ SEQUENCE 964 AA; 109704 MW; 706053000ED85864 CRC64;
 Query Match 58.1%; Score 36; DB 1; Length 964;
 Best Local Similarity 62.5%; Pred. No. 35;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 ATFGTHDG 11
 Db 160 STGTHEG 167

Search completed: August 28, 2003, 18:35:07
 Job time : 6.66667 secs